

# **“On the Analysis of Genome-Wide Association Studies in Family-Based Designs: A Universal, Robust Analysis Approach and an Application to Four Genome-Wide Association Studies”**

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For genome-wide association studies in family-based designs, we propose a new, universally applicable approach. The new test statistic exploits all available information about the association, while, by virtue of its design, it maintains the same robustness against population admixture as traditional family-based approaches that are based exclusively on the within-family information. The approach is suitable for the analysis of almost any trait type, e.g. binary, continuous, time-to-onset, multivariate, etc., and combinations of those. We use simulation studies to verify all theoretically derived properties of the approach, estimate its power, and compare it with other standard approaches. We illustrate the practical implications of the new analysis method by an application to a lung-function phenotype, forced expiratory volume in one second (FEV1) in 4 genome-wide association studies.